

SEQUENCE LISTING

<110> Pangalos, Menelas  
Neefs, Jean-Marc  
Peeters, Danielle

<120> Cloning and Characterisation of Novel Mammalian Peptidases

<130> J0205/7000 (JRV)

<140> 09/743,647

<141> 2001-01-12

<150> GB 9815284.6

<151> 1999-07-14

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<170> PatentIn version 3.0

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Met Gly Gln Leu Asp Ala His Arg Ile Arg Glu Asn Leu Arg Glu Leu
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Leu	Ser	Ile	Tyr	Asp	Asn	Trp	Ile	Arg	Tyr	Phe	Asn	Arg	Ser	Ser	Pro	485	490	495
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Val	Glu	Lys	Phe	Glu	Ala	Glu	Ala	Ala	Ala	Leu	Gly	Gln	Arg	Ile	Ser	625	630	635
Thr	Leu	Gln	Lys	Gly	Ser	Pro	Asp	Pro	Leu	Gln	Val	Arg	Met	Leu	Asn	645	650	655
Asp	Gln	Leu	Met	Leu	Leu	Glu	Arg	Thr	Phe	Leu	Asn	Pro	Arg	Ala	Phe	660	665	670
Pro	Glu	Glu	Arg	Tyr	Tyr	Ser	His	Val	Leu	Trp	Ala	Pro	Ser	His	Gly	675	680	685
Leu	Arg	Ser	His	Ile	Pro	Gly	Leu	Ser	Asn	Ala	Cys	Ser	Arg	Ala	Arg	690	695	700
Asp	Thr	Ala	Ser	Gly	Ser	Glu	Ala	Trp	Ala	Glu	Val	Gln	Arg	Gln	Leu	705	710	715
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<212> PRT

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Asn Leu Arg Glu Leu Ser Lys Glu Pro His Val Ala Thr Ser Ala Arg  
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Asp Glu Ala Leu Val Gln Leu Leu Leu Gly Arg Trp Lys Asp Ser Ala  
85 90 95

Ser Gly Leu Asp Thr Ala Lys Thr Tyr Glu Tyr Thr Val Leu Leu Ser  
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Gly Thr Val Phe His Ser Phe Gln Pro Phe Glu Lys Asn Leu Thr Gly  
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Glu Gln Ala Glu Pro Asn Val Leu Gln Pro Tyr Ala Ala Tyr Ala Pro  
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Pro Gly Thr Pro Lys Gly Pro Leu Val Tyr Ala Asn Arg Gly Ser Glu  
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Ile Ala Leu Thr Arg Tyr Gly Ser Val Gly Arg Gly Ala Lys Ala Ile  
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595 600 605

Gln Glu Asn Leu Gly Ala Leu Leu Glu Ser His Asn Ile Ser Leu Gly  
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Pro Leu Val Thr Ala Val Glu Lys Phe Lys Ala Ala Ala Ala Ala Leu  
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Asn Gln His Ile Leu Thr Leu Gln Lys Ser Ser Pro Asp Pro Leu Gln  
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Val Arg Met Val Asn Asp Gln Leu Met Leu Leu Glu Arg Ala Phe Leu  
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Tyr Gly Gly Val Gly Arg Gly Ala Lys  
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Ser Pro Ala Gln  
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<210> 40

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tctggatgcc gctgtcctca tccagccctg cccttgccac caccagccc agtccccct 180  
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<213> Homo sapiens

<400> 42

Gly Glu Pro Ser Ser Cys Cys Leu His Pro Arg Pro Leu Leu Cys Ser  
1 5 10 15  
Gly Cys Arg Cys Pro His Pro Ala Leu Pro Leu Pro Pro Pro Ser Pro  
20 25 30  
Ala Pro Pro Ala His Leu Ser Leu Ser Ser Gly Ser Leu Pro Leu Phe  
35 40 45  
Leu Trp Pro  
50

<210> 43

<211> 82

<212> DNA

<213> Homo sapiens

<400> 43

gtgaggaggg agacaagggg catcctgaga ccaggacagg agaggctgaa gactgagccc 60

tggccttgtc accttgccgc ag

82

<210> 44

<211> 17

<212> PRT

<213> Homo sapiens

<400> 44

Glu Glu Gly Asp Lys Gly His Pro Glu Thr Arg Thr Gly Glu Ala Glu  
1 5 10 15

Asp

<210> 45

<211> 74

<212> DNA

<213> Homo sapiens

<400> 45

gtatgcacag ccctgaccct gaggtatggg gagccctgca ccccatgac tgagccactg 60

cttgttccctc acag 74

<210> 46

<211> 17

<212> PRT

<213> Homo sapiens

<400> 46

Gly Met His Ser Pro Asp Pro Glu Val Trp Gly Ala Leu His Pro His  
1 5 10 15

Asp

<210> 47

<211> 3110

<212> DNA

<213> Homo sapiens

<400> 47

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caaccacttc tgtgcgctat catcaaagta tacgggtggaa actgggtatcc gaaatgaaag	180
ctgaaaacat caaatcatth cttcgttctt ttacaaagct tcctcatctg gcaggaacag	240
aacaaaattt cttgcttgcc aagaaaatcc aaaccagtg gaagaaattt ggactagatt	300
cagccaagtt ggttcattat gatgtcctct tatcttacc caatgagaca aatgccaaact	360
atatatcgat tgtggatgaa catgaaactg agattttcaa aacatcatac cttgaaccac	420
caccagatgg ctatgagaat gttacaaata ttgtgccacc atataatgct ttctcagccc	480
aaggcatgcc agagggagat cttgtatatg tgaactatgc tcgcactgaa gactttttca	540
aactagaaag agagatgggc atcaactgta ctgggaagat tgttattgca agatatggaa	600
aatcttcag aggaaataaa gttaaaaatg ccatgttagc aggagccata ggaatcatct	660
tgtactcaga tccagctgac tactttgctc ctgaggtaca gccatatccc aaaggatgga	720
atcttctcgg aactgcagcc cagagaggaa atgtgttaaa tttgaatggt gctggtgacc	780
cactcactcc aggctatcca gcaaaagaat acactttcag acttgatggt gaagaaggag	840
tgggaatccc ccgaatacct gtacatccca ttggatataa tgatgcagaa atattattac	900
gctacttggg aggaattgct ccaccagata agagttggaa gggagccctt aatgtgagtt	960
atagtatcgg acctggcttt acagggagtg attctttcag gaaggttaga atgcatgttt	1020
ataacatcaa taaaattaca aggatttaca atgtagtgg aactatcaga ggatctgtgg	1080
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accaaccag tgggggttgct gttttgcaag aaattgcccg gagttttgga aaactgatga	1200
gtaaaggctg gagacctaga agaactatca tttttgccag ctgggatgca gaagaatttg	1260
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ctccccttct ttaccaatta gtgtataaac tgacaaaaga gatccccagc cctgatgatg	1440
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aaaatttgcc tagaatcaat aagctgggat ctggaagtga ctttgaagct tattttcaga	1560

gacttggaat tgcttcaggc agagcccggt acactaagaa taagaaaaca gataagtaca 1620  
gcagctaccc agtgtaccac acaatttatg agacatttga attggtagag aaattttatg 1680  
acccacatt taaaaaaca ctttctgtgg ctcaattacg aggagcactg gtatatgagc 1740  
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tatcatttga ctcttattt tctgctgtga aaaacttctc agaggctgct tcagattttc 1920  
ataaacgact tatacaagtt gatcttaaca atcccattgc agtgagaatg atgaatgacc 1980  
aactgatgct cctggaaaga gcattcatcg atcctcttgg tttaccagga aagctgttct 2040  
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gaatctatga tgctatcttt gatattgaaa ataaagccaa ctctcgtttg gcctggaaag 2160  
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aagaagtatt atagaaggtc tcaagtggct agccattaaa ggtgttgcta aaagtctgag 2280  
gataaaattc acctttctga taacttatga agccagggtg ttctaaactc ttttcatgtc 2340  
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cagaaagtaa aagaaaattc cctaaattat agcaaggaaac atgaattctc agacattgtg 2520  
agtgtgggaa tgtaaaatgg taaaatcact tttgaaaaca gtttggcagt ttcctataaa 2580  
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<210> 48

<211> 740

<212> PRT

<213> Homo sapiens

<400> 48

Met	Ala	Glu	Ser	Arg	Gly	Arg	Leu	Tyr	Leu	Trp	Met	Cys	Leu	Ala	Ala	
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Ala	Leu	Ala	Ser	Phe	Leu	Met	Gly	Phe	Met	Val	Gly	Trp	Phe	Ile	Lys	
			20					25					30			
Pro	Leu	Lys	Glu	Thr	Thr	Thr	Ser	Val	Arg	Tyr	His	Gln	Ser	Ile	Arg	
		35					40					45				
Trp	Lys	Leu	Val	Ser	Glu	Met	Lys	Ala	Glu	Asn	Ile	Lys	Ser	Phe	Leu	
	50					55					60					
Arg	Ser	Phe	Thr	Lys	Leu	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe	
65					70					75					80	
Leu	Leu	Ala	Lys	Lys	Ile	Gln	Thr	Gln	Trp	Lys	Lys	Phe	Gly	Leu	Asp	
				85					90					95		
Ser	Ala	Lys	Leu	Val	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Glu	
			100					105						110		
Thr	Asn	Ala	Asn	Tyr	Ile	Ser	Ile	Val	Asp	Glu	His	Glu	Thr	Glu	Ile	
		115					120					125				
Phe	Lys	Thr	Ser	Tyr	Leu	Glu	Pro	Pro	Pro	Asp	Gly	Tyr	Glu	Asn	Val	
	130					135					140					
Thr	Asn	Ile	Val	Pro	Pro	Tyr	Asn	Ala	Phe	Ser	Ala	Gln	Gly	Met	Pro	
145					150					155					160	
Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	
			165						170					175		
Lys	Leu	Glu	Arg	Glu	Met	Gly	Ile	Asn	Cys	Thr	Gly	Lys	Ile	Val	Ile	
			180					185					190			
Ala	Arg	Tyr	Gly	Lys	Ile	Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Met	
		195					200						205			
Leu	Ala	Gly	Ala	Ile	Gly	Ile	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	
	210					215					220					
Phe	Ala	Pro	Glu	Val	Gln	Pro	Tyr	Pro	Lys	Gly	Trp	Asn	Leu	Pro	Gly	
225					230					235					240	
Thr	Ala	Ala	Gln	Arg	Gly	Asn	Val	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	
				245				250						255		
Pro	Leu	Thr	Pro	Gly	Tyr	Pro	Ala	Lys	Glu	Tyr	Thr	Phe	Arg	Leu	Asp	
			260					265					270			
Val	Glu	Glu	Gly	Val	Gly	Ile	Pro	Arg	Ile	Pro	Val	His	Pro	Ile	Gly	
		275					280					285				

Tyr Asn Asp Ala Glu Ile Leu Leu Arg Tyr Leu Gly Gly Ile Ala Pro  
 290 295 300  
 Pro Asp Lys Ser Trp Lys Gly Ala Leu Asn Val Ser Tyr Ser Ile Gly  
 305 310 315 320  
 Pro Gly Phe Thr Gly Ser Asp Ser Phe Arg Lys Val Arg Met His Val  
 325 330 335  
 Tyr Asn Ile Asn Lys Ile Thr Arg Ile Tyr Asn Val Val Gly Thr Ile  
 340 345 350  
 Arg Gly Ser Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg  
 355 360 365  
 Asp Ser Trp Val Phe Gly Ala Ile Asp Pro Thr Ser Gly Val Ala Val  
 370 375 380  
 Leu Gln Glu Ile Ala Arg Ser Phe Gly Lys Leu Met Ser Lys Gly Trp  
 385 390 395 400  
 Arg Pro Arg Arg Thr Ile Ile Phe Ala Ser Trp Asp Ala Glu Glu Phe  
 405 410 415  
 Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Val Lys Ile Leu  
 420 425 430  
 Gln Glu Arg Ser Ile Ala Tyr Ile Asn Ser Asp Ser Ser Ile Glu Gly  
 435 440 445  
 Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Leu Tyr Gln Leu Val  
 450 455 460  
 Tyr Lys Leu Thr Lys Glu Ile Pro Ser Pro Asp Asp Gly Phe Glu Ser  
 465 470 475 480  
 Lys Ser Leu Tyr Glu Ser Trp Leu Glu Lys Asp Pro Ser Pro Glu Asn  
 485 490 495  
 Lys Asn Leu Pro Arg Ile Asn Lys Leu Gly Ser Gly Ser Asp Phe Glu  
 500 505 510  
 Ala Tyr Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr  
 515 520 525  
 Lys Asn Lys Lys Thr Asp Lys Tyr Ser Ser Tyr Pro Val Tyr His Thr  
 530 535 540  
 Ile Tyr Glu Thr Phe Glu Leu Val Glu Lys Phe Tyr Asp Pro Thr Phe  
 545 550 555 560  
 Lys Lys Gln Leu Ser Val Ala Gln Leu Arg Gly Ala Leu Val Tyr Glu  
 565 570 575  
 Leu Val Asp Ser Lys Ile Ile Pro Phe Asn Ile Gln Asp Tyr Ala Glu  
 580 585 590  
 Ala Leu Lys Asn Tyr Ala Ala Ser Ile Tyr Asn Leu Ser Lys Lys His

595		600		605
Asp Gln Gln Leu Thr Asp His Gly Val Ser Phe Asp Ser Leu Phe Ser				
610		615		620
Ala Val Lys Asn Phe Ser Glu Ala Ala Ser Asp Phe His Lys Arg Leu				
625		630		635
Ile Gln Val Asp Leu Asn Asn Pro Ile Ala Val Arg Met Met Asn Asp				
	645		650	655
Gln Leu Met Leu Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro				
	660		665	670
Gly Lys Leu Phe Tyr Arg His Ile Ile Phe Ala Pro Ser Ser His Asn				
	675		680	685
Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Ile Phe Asp				
	690		695	700
Ile Glu Asn Lys Ala Asn Ser Arg Leu Ala Trp Lys Glu Val Lys Lys				
705		710		715
His Ile Ser Ile Ala Ala Phe Thr Ile Gln Ala Ala Ala Gly Thr Leu				
	725		730	735
Lys Glu Val Leu				
	740			

<210> 49

<211> 1860

<212> DNA

<213> Homo sapiens

<400> 49

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aaaaatgaaa ttccttatct tcgcattttt cggtggtggt caccttttat cctgtgctc	180
tgggaaagct atatgcaaga atggcatctc taagaggact tttgaagaaa taaaagaaga	240
aatagccagc tgtggagatg ttgctaaagc aatcatcaac ctagctgttt atggtaaagc	300
ccagaacaga tcctatgagc gattggcact tctggttgat actgttggaac ccagactgag	360
tggtctcaag aacctagaaa aagccatcca aattatgtac caaaacctgc agcaagatgg	420
gctggagaaa gttcacctgg agccagtga aatacccccac tgggagaggg gagaagaatc	480
agctgtgatg ctggagccaa gaattcataa gatagccatc ctgggtcttg gcagcagcat	540
tgggactcct ccagaaggca ttacagcaga agttctggtg gtgacctctt tcgatgaact	600



gcagagaagg gcctcagaag caagagggaa gattgttggt tataaccaac cttacatcaa 660  
ctactcaagg acggtgcaat accgaacgca gggggcggtg gaagctgcca aggttggggc 720  
tttggcatct ctcatctgat ccgtggcctc cttctccatc tacagtctc acacaggtat 780  
tcaggaatac caggatggcg tgcccaagat tccaacagcc tgtattacgg tggaagatgc 840  
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ggtgatggag tctgacgcag gaaccttctt acccactggg ctgcaattca ctggcagtga 1260  
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ctttcttgat actttccaaa ttctctgatt ctagaaaaag gaatcattct cccctccctc 1740  
ccaccacata gaatcaacat atggtaggga ttacagtggg ggcatttctt tatatcacct 1800  
cttaaaaaca ttgtttccac tttaaaagta aacacttaat aaatttttgg aagatctctg 1860

<210> 50

<211> 472

<212> PRT

<213> Homo sapiens

<400> 50

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser  
1 5 10 15

Leu	Cys	Ser	Gly	Lys	Ala	Ile	Cys	Lys	Asn	Gly	Ile	Ser	Lys	Arg	Thr	20	25	30
Phe	Glu	Glu	Ile	Lys	Glu	Glu	Ile	Ala	Ser	Cys	Gly	Asp	Val	Ala	Lys	35	40	45
Ala	Ile	Ile	Asn	Leu	Ala	Val	Tyr	Gly	Lys	Ala	Gln	Asn	Arg	Ser	Tyr	50	55	60
Glu	Arg	Leu	Ala	Leu	Leu	Val	Asp	Thr	Val	Gly	Pro	Arg	Leu	Ser	Gly	65	70	75
Ser	Lys	Asn	Leu	Glu	Lys	Ala	Ile	Gln	Ile	Met	Tyr	Gln	Asn	Leu	Gln	85	90	95
Gln	Asp	Gly	Leu	Glu	Lys	Val	His	Leu	Glu	Pro	Val	Arg	Ile	Pro	His	100	105	110
Trp	Glu	Arg	Gly	Glu	Glu	Ser	Ala	Val	Met	Leu	Glu	Pro	Arg	Ile	His	115	120	125
Lys	Ile	Ala	Ile	Leu	Gly	Leu	Gly	Ser	Ser	Ile	Gly	Thr	Pro	Pro	Glu	130	135	140
Gly	Ile	Thr	Ala	Glu	Val	Leu	Val	Val	Thr	Ser	Phe	Asp	Glu	Leu	Gln	145	150	155
Arg	Arg	Ala	Ser	Glu	Ala	Arg	Gly	Lys	Ile	Val	Val	Tyr	Asn	Gln	Pro	165	170	175
Tyr	Ile	Asn	Tyr	Ser	Arg	Thr	Val	Gln	Tyr	Arg	Thr	Gln	Gly	Ala	Val	180	185	190
Glu	Ala	Ala	Lys	Val	Gly	Ala	Leu	Ala	Ser	Leu	Ile	Arg	Ser	Val	Ala	195	200	205
Ser	Phe	Ser	Ile	Tyr	Ser	Pro	His	Thr	Gly	Ile	Gln	Glu	Tyr	Gln	Asp	210	215	220
Gly	Val	Pro	Lys	Ile	Pro	Thr	Ala	Cys	Ile	Thr	Val	Glu	Asp	Ala	Glu	225	230	235
Met	Met	Ser	Arg	Met	Ala	Ser	His	Gly	Ile	Lys	Ile	Val	Ile	Gln	Leu	245	250	255
Lys	Met	Gly	Ala	Lys	Thr	Tyr	Pro	Asp	Thr	Asp	Ser	Phe	Asn	Thr	Val	260	265	270
Ala	Glu	Ile	Thr	Gly	Ser	Lys	Tyr	Pro	Glu	Gln	Val	Val	Leu	Val	Ser	275	280	285
Gly	His	Leu	Asp	Ser	Trp	Asp	Val	Gly	Gln	Gly	Ala	Met	Asp	Asp	Gly	290	295	300
Gly	Gly	Ala	Phe	Ile	Ser	Trp	Glu	Ala	Leu	Ser	Leu	Ile	Lys	Asp	Leu	305	310	315
Gly	Leu	Arg	Pro	Lys	Arg	Thr	Leu	Arg	Leu	Val	Leu	Trp	Thr	Ala	Glu	325	330	335

Glu Gln Gly Gly Val Gly Ala Phe Gln Tyr Tyr Gln Leu His Lys Val  
340 345 350  
Asn Ile Ser Asn Tyr Ser Leu Val Met Glu Ser Asp Ala Gly Thr Phe  
355 360 365  
Leu Pro Thr Gly Leu Gln Phe Thr Gly Ser Glu Lys Ala Arg Ala Ile  
370 375 380  
Met Glu Glu Val Met Ser Leu Leu Gln Pro Leu Asn Ile Thr Gln Val  
385 390 395 400  
Leu Ser His Gly Glu Gly Thr Asp Ile Asn Phe Trp Ile Gln Ala Gly  
405 410 415  
Val Pro Gly Ala Ser Leu Leu Asp Asp Leu Tyr Lys Tyr Phe Phe Phe  
420 425 430  
His His Ser His Gly Asp Thr Met Thr Val Met Asp Pro Lys Gln Met  
435 440 445  
Asn Val Ala Ala Ala Val Trp Ala Val Val Ser Tyr Val Val Ala Asp  
450 455 460  
Met Glu Glu Met Leu Pro Arg Ser  
465 470

<210> 51

<211> 750

<212> PRT

<213> Homo sapiens

<400> 51

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg  
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Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe  
20 25 30  
Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu  
35 40 45  
Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu  
50 55 60  
Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His Asn Phe Thr Gln Ile  
65 70 75 80  
Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile  
85 90 95  
Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His

100					105					110					
Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile
		115					120					125			
Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe
	130					135					140				
Glu	Pro	Pro	Pro	Pro	Gly	Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro
145					150					155					160
Phe	Ser	Ala	Phe	Ser	Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr
				165					170					175	
Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met
			180					185					190		
Lys	Ile	Asn	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val
		195					200					205			
Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly
	210					215					220				
Val	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys
225					230					235					240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly
				245					250					255	
Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr
			260					265					270		
Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	Ala	Val	Gly
		275					280					285			
Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys
	290					295					300				
Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg
305					310					315					320
Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn
				325					330					335	
Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val
			340					345					350		
Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro
		355					360					365			
Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly
	370					375					380				
Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg
385					390					395					400
Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile
				405					410					415	

Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	420	425	430
Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	435	440	445
Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val	450	455	460
Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu	465	470	480
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu	Ser	485	490	495
Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	Arg	Ile	500	505	510
Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln	Arg	Leu	515	520	525
Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Glu	Thr	Asn	530	535	540
Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr	Tyr	Glu	545	550	560
Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	Lys	Tyr	His	Leu	Thr	Val	565	570	575
Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser	Ile	Val	580	585	590
Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	595	600	605
Asp	Lys	Ile	Tyr	Ser	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	610	615	620
Tyr	Ser	Val	Ser	Phe	Asp	Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	625	630	635
Glu	Ile	Ala	Ser	Lys	Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	645	650	655
Asn	Pro	Ile	Val	Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	660	665	670
Arg	Ala	Phe	Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	675	680	685
His	Val	Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	690	695	700
Phe	Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp	705	710	720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala	Ala	725	730	735

Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala  
740 745 750

<210> 52

<211> 265

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 52

Thr Lys His Thr Val Ala Thr Val Gly Val Pro Tyr Lys Val Gly Lys  
1 5 10 15

Lys Leu Ile Ala Asn Ile Ala Leu Asn Ile Asp Tyr Ser Leu Tyr Phe  
20 25 30

Ala Met Asp Ser Tyr Val Glu Phe Ile Lys Thr Gln Asn Ile Ile Ala  
35 40 45

Asp Thr Lys His Gly Asp Pro Asp Asn Ile Val Ala Leu Gly Ala His  
50 55 60

Ser Asp Ser Val Glu Glu Gly Pro Gly Ile Asn Asp Asp Gly Ser Gly  
65 70 75 80

Thr Ile Ser Leu Leu Asn Val Ala Lys Gln Leu Thr His Phe Lys Ile  
85 90 95

Asn Asn Lys Val Arg Phe Ala Trp Trp Ala Ala Glu Glu Glu Gly Leu  
100 105 110

Leu Gly Ser Asn Phe Tyr Ala Tyr Asn Leu Thr Lys Glu Glu Asn Ser  
115 120 125

Lys Ile Arg Val Phe Met Asp Tyr Asp Met Met Ala Ser Pro Asn Tyr  
130 135 140

Glu Tyr Glu Ile Tyr Asp Ala Asn Asn Lys Glu Asn Pro Lys Gly Ser  
145 150 155 160

Glu Glu Leu Lys Asn Leu Tyr Val Asp Tyr Tyr Lys Ala His His Leu  
165 170 175

Asn Tyr Thr Leu Val Pro Phe Asp Gly Arg Ser Asp Tyr Val Gly Phe  
180 185 190

Ile Asn Asn Gly Ile Pro Ala Gly Gly Ile Ala Thr Gly Ala Glu Lys  
195 200 205

Asn Asn Val Asn Asn Gly Lys Val Leu Asp Arg Cys Tyr His Gln Leu  
210 215 220

Cys Asp Asp Val Ser Asn Leu Ser Trp Asp Ala Phe Ile Thr Asn Thr

225		230		235		240									
Lys	Leu	Ile	Ala	His	Ser	Val	Ala	Thr	Tyr	Ala	Asp	Ser	Phe	Glu	Gly
				245					250					255	

Phe	Pro	Lys	Arg	Glu	Thr	Gln	Lys	His
			260					265

<210> 53

<211> 268

<212> PRT

<213> Vibrio cholerae

<400> 53

Gln	Ile	Thr	Asn	Thr	Ile	Arg	Ala	Leu	Ser	Ser	Phe	Asn	Asn	Arg	Phe
1				5					10					15	

Tyr	Thr	Thr	Ala	Ser	Gly	Ala	Gln	Ala	Ser	Asp	Trp	Leu	Ala	Asn	Glu
			20					25					30		

Trp	Arg	Ser	Leu	Ile	Ser	Ser	Leu	Pro	Gly	Ser	Arg	Ile	Glu	Gln	Ile
		35					40					45			

Lys	His	Ser	Gly	Tyr	Asn	Gln	Lys	Ser	Val	Val	Leu	Thr	Ile	Gln	Gly
	50					55					60				

Ser	Glu	Lys	Pro	Asp	Glu	Trp	Val	Ile	Val	Gly	Gly	His	Leu	Asp	Ser
65					70					75					80

Thr	Leu	Gly	Ser	His	Thr	Asn	Glu	Gln	Ser	Ile	Ala	Pro	Gly	Ala	Asp
				85					90					95	

Asp	Asp	Ala	Ser	Gly	Ile	Ala	Ser	Leu	Ser	Glu	Ile	Ile	Arg	Val	Leu
			100					105					110		

Arg	Asp	Asn	Asn	Phe	Arg	Pro	Lys	Arg	Ser	Ala	Ala	Leu	Met	Ala	Tyr
		115					120					125			

Ala	Ala	Glu	Glu	Val	Gly	Leu	Arg	Gly	Ser	Gln	Asp	Pro	Ala	Asn	Gln
	130					135					140				

Tyr	Lys	Ala	Gln	Gly	Lys	Lys	Val	Val	Ser	Val	Leu	Gln	Leu	Asp	Met
145					150					155					160

Thr	Asn	Tyr	Arg	Gly	Ser	Ala	Glu	Asp	Ile	Val	Phe	Ile	Thr	Asp	Tyr
				165					170					175	

Thr	Asp	Ser	Asn	Leu	Thr	Gln	Phe	Leu	Thr	Thr	Leu	Ile	Asp	Glu	Tyr
			180					185					190		

Leu	Pro	Glu	Leu	Thr	Tyr	Gly	Tyr	Asp	Arg	Cys	Gly	Tyr	Ala	Cys	Ser
		195					200					205			

Asp His Ala Ser Trp His Lys Ala Gly Phe Ser Ala Ala Met Pro Phe  
210 215 220  
Glu Ser Lys Phe Lys Asp Tyr Asn Pro Lys Ile His Thr Ser Gln Asp  
225 230 235 240  
Thr Leu Ala Asn Ser Asp Pro Thr Gly Asn His Ala Val Thr Phe Thr  
245 250 255  
Lys Leu Gly Leu Ala Tyr Val Ile Glu Met Ala Asn  
260 265

<210> 54

<211> 268

<212> PRT

<213> Aeromonas proteolytica

<400> 54

Gln Ile Thr Gly Thr Ile Ser Ser Leu Glu Ser Phe Thr Asn Arg Phe  
1 5 10 15  
Tyr Thr Thr Thr Ser Gly Ala Gln Ala Ser Asp Trp Ile Ala Ser Glu  
20 25 30  
Trp Gln Ala Leu Ser Ala Ser Leu Pro Asn Ala Ser Val Lys Gln Val  
35 40 45  
Ser His Ser Gly Tyr Asn Gln Lys Ser Val Val Met Thr Ile Thr Gly  
50 55 60  
Ser Glu Ala Pro Asp Glu Trp Ile Val Ile Gly Gly His Leu Asp Ser  
65 70 75 80  
Thr Ile Gly Ser His Thr Asn Glu Gln Ser Val Ala Pro Gly Ala Asp  
85 90 95  
Asp Asp Ala Ser Gly Ile Ala Ala Val Thr Glu Val Ile Arg Val Leu  
100 105 110  
Ser Glu Asn Asn Phe Gln Pro Lys Arg Ser Ile Ala Phe Met Ala Tyr  
115 120 125  
Ala Ala Glu Glu Val Gly Leu Arg Gly Ser Gln Asp Leu Ala Asn Gln  
130 135 140  
Tyr Lys Ser Glu Gly Lys Asn Val Val Ser Ala Leu Gln Leu Asp Met  
145 150 155 160  
Thr Asn Tyr Lys Gly Ser Ala Gln Asp Val Val Phe Ile Thr Asp Tyr  
165 170 175  
Thr Asp Ser Asn Phe Thr Gln Tyr Leu Thr Gln Leu Met Asp Glu Tyr  
180 185 190



Leu Pro Ser Leu Thr Tyr Gly Phe Asp Thr Cys Gly Tyr Ala Cys Ser  
195 200 205

Asp His Ala Ser Trp His Asn Ala Gly Tyr Pro Ala Ala Met Pro Phe  
210 215 220

Glu Ser Lys Phe Asn Asp Tyr Asn Pro Arg Ile His Thr Thr Gln Asp  
225 230 235 240

Thr Leu Ala Asn Ser Asp Pro Thr Gly Ser His Ala Lys Lys Phe Thr  
245 250 255

Gln Leu Gly Leu Ala Tyr Ala Ile Glu Met Gly Ser  
260 265

<210> 55

<211> 263

<212> PRT

<213> Streptomyces griseus

<400> 55

Asn Asn Gly Gly Asn Arg Ala His Gly Arg Pro Gly Tyr Lys Ala Ser  
1 5 10 15

Val Asp Tyr Val Lys Ala Lys Leu Asp Ala Ala Gly Tyr Thr Thr Thr  
20 25 30

Leu Gln Gln Phe Thr Ser Gly Gly Ala Thr Gly Tyr Asn Leu Ile Ala  
35 40 45

Asn Trp Pro Gly Gly Asp Pro Asn Lys Val Leu Met Ala Gly Ala His  
50 55 60

Leu Asp Ser Val Ser Ser Gly Ala Gly Ile Asn Asp Asn Gly Ser Gly  
65 70 75 80

Ser Ala Ala Val Leu Glu Thr Ala Leu Ala Val Ser Arg Ala Gly Tyr  
85 90 95

Gln Pro Asp Lys His Leu Arg Phe Ala Trp Trp Gly Ala Glu Glu Leu  
100 105 110

Gly Leu Ile Gly Ser Lys Phe Tyr Val Asn Asn Leu Pro Ser Ala Asp  
115 120 125

Arg Ser Lys Leu Ala Gly Tyr Leu Asn Phe Asp Met Ile Gly Ser Pro  
130 135 140

Asn Pro Gly Tyr Phe Val Tyr Asp Asp Asp Pro Val Ile Glu Lys Thr  
145 150 155 160

Phe Lys Asn Tyr Phe Ala Gly Leu Asn Val Pro Thr Glu Ile Glu Thr

				165						170						175
Glu	Gly	Asp	Gly	Arg	Ser	Asp	His	Ala	Pro	Phe	Lys	Asn	Val	Gly	Val	
			180					185					190			
Pro	Val	Gly	Gly	Leu	Phe	Thr	Gly	Ala	Gly	Tyr	Thr	Lys	Ser	Ala	Ala	
		195					200					205				
Gln	Ala	Gln	Lys	Trp	Gly	Gly	Thr	Ala	Gly	Gln	Ala	Phe	Asp	Arg	Cys	
	210					215					220					
Tyr	His	Ser	Ser	Cys	Asp	Ser	Leu	Ser	Asn	Ile	Asn	Asp	Thr	Ala	Leu	
225					230					235					240	
Asp	Arg	Asn	Ser	Asp	Ala	Ala	Ala	His	Ala	Ile	Trp	Thr	Leu	Ser	Ser	
				245					250						255	
Gly	Thr	Gly	Glu	Pro	Pro	Thr										
			260													

<210> 56

<211> 282

<212> PRT

<213> Homo sapiens

<400> 56

Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp
1				5					10					15	
Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly
			20					25					30		
Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser
		35					40					45			
Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly
	50					55					60				
Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser
65					70					75				80	
Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His
				85					90					95	
Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro
			100					105					110		
Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu
		115					120						125		
Leu	Gly	Ser	Thr	Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu
	130					135					140				

Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr  
145 150 155 160  
Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn  
165 170 175  
Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser  
180 185 190  
Leu Tyr Glu Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly  
195 200 205  
Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe  
210 215 220  
Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn  
225 230 235 240  
Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr  
245 250 255  
Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr  
260 265 270  
His Leu Thr Val Ala Gln Val Arg Gly Gly  
275 280

<210> 57

<211> 282

<212> PRT

<213> Homo sapiens

<400> 57

Asp Ala Glu Ile Leu Leu Arg Tyr Leu Gly Gly Ile Ala Pro Pro Asp  
1 5 10 15  
Lys Ser Trp Lys Gly Ala Leu Asn Val Ser Tyr Ser Ile Gly Pro Gly  
20 25 30  
Phe Thr Gly Ser Asp Ser Phe Arg Lys Val Arg Met His Val Tyr Asn  
35 40 45  
Ile Asn Lys Ile Thr Arg Ile Tyr Asn Val Val Gly Thr Ile Arg Gly  
50 55 60  
Ser Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser  
65 70 75 80  
Trp Val Phe Gly Ala Ile Asp Pro Thr Ser Gly Val Ala Val Leu Gln  
85 90 95  
Glu Ile Ala Arg Ser Phe Gly Lys Leu Met Ser Lys Gly Trp Arg Pro  
100 105 110

Arg Arg Thr Ile Ile Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu  
115 120 125

Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Val Lys Ile Leu Gln Glu  
130 135 140

Arg Ser Ile Ala Tyr Ile Asn Ser Asp Ser Ser Ile Glu Gly Asn Tyr  
145 150 155 160

Thr Leu Arg Val Asp Cys Thr Pro Leu Leu Tyr Gln Leu Val Tyr Lys  
165 170 175

Leu Thr Lys Glu Ile Pro Ser Pro Asp Asp Gly Phe Glu Ser Lys Ser  
180 185 190

Leu Tyr Glu Ser Trp Leu Glu Lys Asp Pro Ser Pro Glu Asn Lys Asn  
195 200 205

Leu Pro Arg Ile Asn Lys Leu Gly Ser Gly Ser Asp Phe Glu Ala Tyr  
210 215 220

Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn  
225 230 235 240

Lys Lys Thr Asp Lys Tyr Ser Ser Tyr Pro Val Tyr His Thr Ile Tyr  
245 250 255

Glu Thr Phe Glu Leu Val Glu Lys Phe Tyr Asp Pro Thr Phe Lys Lys  
260 265 270

Gln Leu Ser Val Ala Gln Leu Arg Gly Ala  
275 280

<210> 58

<211> 283

<212> PRT

<213> Homo sapiens

<400> 58

Arg Asp Leu Leu Cys Asn Leu Asn Gly Thr Leu Ala Pro Ala Thr Trp  
1 5 10 15

Gln Gly Ala Leu Gly Cys His Tyr Arg Leu Gly Pro Gly Phe Arg Pro  
20 25 30

Asp Gly Asp Phe Pro Ala Asp Ser Gln Val Asn Val Ser Val Tyr Asn  
35 40 45

Arg Leu Glu Leu Arg Asn Ser Ser Asn Val Leu Gly Ile Ile Arg Gly  
50 55 60

Ala Val Glu Pro Asp Arg Tyr Val Leu Tyr Gly Asn His Arg Asp Ser

65		70		75		80
Trp Val His Gly	Ala Val Asp Pro Ser Ser Gly Thr Ala Val Leu Leu	85	90	95		
Glu Leu Ser Arg	Val Leu Gly Thr Leu Leu Lys Lys Gly Thr Trp Arg	100	105	110		
Pro Arg Arg Ser	Ile Val Phe Ala Ser Trp Gly Ala Glu Glu Phe Gly	115	120	125		
Leu Ile Gly Ser	Thr Glu Phe Thr Glu Glu Phe Phe Asn Lys Leu Gln	130	135	140		
Glu Arg Thr Val	Ala Tyr Ile Asn Val Asp Ile Ser Val Phe Ala Asn	145	150	155	160	
Ala Thr Leu Arg	Val Gln Gly Thr Pro Pro Val Gln Ser Val Val Phe	165	170	175		
Ser Ala Thr Lys	Glu Ile Arg Ser Pro Gly Pro Gly Asp Leu Ser Ile	180	185	190		
Tyr Asp Asn Trp	Ile Arg Tyr Phe Asn Arg Ser Ser Pro Val Tyr Gly	195	200	205		
Leu Val Pro Ser	Leu Gly Ser Leu Gly Ala Gly Ser Asp Tyr Ala Pro	210	215	220		
Phe Val His Phe	Leu Gly Ile Ser Ser Met Asp Ile Ala Tyr Thr Tyr	225	230	235	240	
Asp Arg Ser Lys	Thr Ser Ala Arg Ile Tyr Pro Thr Tyr His Thr Ala	245	250	255		
Phe Asp Thr Phe	Asp Tyr Val Asp Lys Phe Leu Asp Pro Gly Phe Ser	260	265	270		
Ser His Gln Ala	Val Ala Arg Thr Ala Gly Ser	275	280			

<210> 59

<211> 259

<212> PRT

<213> Homo sapiens

<400> 59

Ser Pro His Thr	Gly Ile Gln Glu Tyr Gln Asp Gly Val Pro Lys Ile	1	5	10	15
Pro Thr Ala Cys	Ile Thr Val Glu Asp Ala Glu Met Met Ser Arg Met	20	25	30	

[illegible]

FIG. 8.

NAALAD I DAQKLEKNGSAPPD-SSURGSLKVPINVGPGFTGNF---STQKVKEHIHSTNEVTRIVNIGTLRGAVEPDRYVILGG 375  
 NAALAD II DAEILLRYLGGIAPPD-KSUKGALNVSSIGPGFTGSD---SFRKVRCHVYNINKITRIYVVGTLRGAVEPDRYVILGG 366  
 NAALAD L --RDLLCNLNGTLAP--ATUQGALGCHYRLGPGFRPDGPADSQVNVSVYNRLELRNSSNULGIIRGAVEPDRYVILGN 367  
 NAALAD IV SPHTGQIEYQDGVKPIKTACITVEDAEHNSRHASHGIK---IVIQLKCAKTYPD TDS-FNVAEITGSKYPEQVVLVSG 289  
 APE 3 yeast -----TKHTVATVGVPYKVGKKLIANIALNIDYSLYFANDSYVEFIKTQLIADTKHG-DPILNIVLALGA 313  
 P96152 QITNTIRALSSFNRFYTTASGAQASDMLANEURSLIS---SLPGSRHEQIKHSGVNO-KSVULTIQSEKPDDEVIVGG 199  
 AMPX vibpr QITGTSSLESFTNRFYTTTSGAQASDMLIASEUQALSA---SLPNASVKQVSHSGVNO-KSVNHTITGSEAPDEVIVILGG 202  
 APX Strgr -----NNGGNR--AHGRPGYKASVDYVKAKLDA--GYTTTQQFTSGGATG-YMLIANUPCG-DPNKVLHAGA 84

NAALAD I HRDSU-VF-----G-I-DPQSG-NAV-VHEVMSFGTL-KKEG-RRPRRTILASMDNEEFGLLGSTEMA-EE-NS 439  
 NAALAD II HRDSU-VF-----G-AI-DPTSG-VAV-LOEHLNDSFGKL-HSKG-RRPRRTILASMDNEEFGLLGSTEMA-EE-NV 429  
 NAALAD L HRDSU-VH-----GAV--DPSGTVL-L-ELSEVLTLLK-KGTWPPRSIVASMGREEFGLIGSTEFT-EEFFN 432  
 NAALAD IV HLDSNDV-----CGAMDGCG-APISU-EALSLL-----KDLG-LRPHRTLRVLTREECGGVCFAQY-QLHKV 352  
 APE 3 yeast HSDS--VEE-----EPGINDDGGCTISL-L-NVLRQLTH-----FKNNKVRFAUMANEELGLGSENFAYNLTK 375  
 P96152 HLDS--VSS-----GAGINDNGSGSNAV-L-ETALAV-----RDNN-FRPRSAALHNAVANEVGLRGSDPA-NQYKA 270  
 AMPX vibpr HLDS--VSS-----GAGINDNGSGSNAV-L-ETALAV-----SENN-FQPKRSIAFMANANEVGLRGSDLA-NQYKS 273  
 APX Strgr HLDS--VSS-----GAGINDNGSGSNAV-L-ETALAV-----SRAG-FQPKRSIAFMANANEVGLRGSDLA-NQYKS 147

NAALAD I RLLQERGVAYINADSSI-EGNYTLRQDCPLHYSLVHNLKELKSPDECFEGKSLYESUTKKS--PSPEFSGHPRISKLG 516  
 NAALAD II KILQERSIAYINADSSI-EGNYTLRQDCPLLYQLVYKLVKEIPSPDDGCFESKSLYESULEKD--PSPENKNLPRINKLG 506  
 NAALAD L KL-QEPTVAYINADISV-FANATLRQCPPPVQSVVFSANKEIRSPGPGD--LSIYDNTIRYFNRRSSPVYGLVPSLGSLS 508  
 NAALAD IV NIS--NYSLVNESAGT-FLPTGLOFTCEKARA---INEEVH-----SLQPLNITQ-----VLSHG 404  
 APE 3 yeast ENSKIR--VFDDYDMMHMA-SPNYEVEHYDANKENP--KGEELK-----NLVVDYVYKAH-----HLNYTLVPFDG 435  
 P96152 QGK--KQVSVQLQDMTNYRGSIEDIFIDYDTS---NLIQFLT-----TLIDEVLPEL-----TYG-----YDRCG 327  
 AMPX vibpr EGK--NVVSALQLDHTNYKGSADVVFIIDYDTS---NFIQYLT-----QLHDESLPSL-----TYG-----FDTGG 330  
 APX Strgr AD-RSLAGYLNFM-IGSPNPGYFYDDDPVIEK--TFKNYFAG-----LNVPTETETE-----GDGRSDHAPFKN 210

FIG. 8. (CONTINUED)

NAALAD I	★	SGNDFEVF	QRL	IASGRARYT	NUETNKF	SGYPLYH	SVYEL	VEK	---	FYDPH	KYH	---	LTV	QVRGG	---	582	
NAALAD II		SGSDFEAY	QRL	IASGRARYT	NKKTKYSS	YPVYH	YIYEF	VEK	---	FYDPT	KKQ	---	LSV	QLRGA	---	572	
NAALAD L		AGSDYAPF	VHFL	ISSHDIA	YTYDRSKT	SARIYPT	YHAFD	FDYVDK	---	FLDPG	SSH	---	QAV	RTAGS	---	574	
NAALAD IV		EGTDIN	---	FQ	IQACVPGAS	LLDDL	YKYFF	---	---	FHS	HGD	---	MTV	DPKQMN	VAALV	---	472
APX 3 yeast		RSDYVGF	INNGIP	AGGIATGA	EKNVNN	NGKVL	DRCYH	QLCDD	VSN	---	SUDAF	---	ITNTK	LIAHSV	ATV	---	515
P96152		YACSDHAS	---	CHKAC	FSAHP	ES	PKF	---	---	---	---	---	---	---	---	---	391
AMPX vibpr		YACSDHAS	---	CHNAC	YPAAHP	ES	PKF	---	---	---	---	---	---	---	---	---	394
APX strgr		VGVPVGG	---	LTGA	YTKSAA	QAQ	---	---	---	---	---	---	---	---	---	---	284